

#30/Jul
09-19-01
1752RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/403,803ADATE: 07/20/2001
TIME: 13:26:03Input Set : A:\41426-A-PCT-US.txt
Output Set: N:\CRF3\07202001\H403803A.raw

3 <110> APPLICANT: Ron S. Israeli et al.
 5 <120> TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
 7 <130> FILE REFERENCE: 1769/41426-C/JPW/SHS
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/08/403,803A
 C--> 9 <141> CURRENT FILING DATE: 1999-10-26
 9 <160> NUMBER OF SEQ ID NOS: 38
 11 <170> SOFTWARE: PatentIn version 3.0
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 2653
 15 <212> TYPE: DNA
 16 <213> ORGANISM: human
 18 <400> SEQUENCE: 1

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23	gcgaattcca	gcctgcagg	ctgataagcg	aggcattagt	gagattgaga	gagactttac	180
25	cccgcctg	tggttgagg	gcgcgcagta	gagcagcagc	acaggcgcgg	gtcccgggag	240
27	cccgcctctg	ctcgcgcga	gatgtggaat	ctccttcacg	aaaccgactc	ggctgtggcc	300
29	accgcgcgcc	gccgcgcctg	gctgtgcgct	ggggcgctgg	tgctggcggg	tggcttcttt	360
31	ctcctcgct	tcctcttcgg	gtggtttata	aaatcctcca	atgaagctac	taacattact	420
33	ccaaagcata	atatgaaagc	atttttggat	gaattgaaag	ctgagaacat	caagaagtgc	480
35	ttatataatt	ttacacagat	accacattta	gcaggaacag	aacaaaactt	tcagcttgca	540
37	aagcaaattc	aatcccagtg	gaaagaattt	ggcctggatt	ctggttgagct	agcacattat	600
39	gatgtcctgt	tgtcctaccc	aaataagact	catcccaact	acatctcaat	aattaatgaa	660
41	gatggaaatg	agattttcaa	cacatcatta	tttgaaccac	ctcctccagg	atatgaaaat	720
43	gtttcggata	ttgtaccacc	tttcagtgt	ttctctctc	aaggaatgcc	agagggcgat	780
45	ctagtgtatg	ttactatgc	acgaactgaa	gacttcttta	aattggaacg	ggacatgaaa	840
47	atcaattgct	ctgggaaaat	tgtaattgcc	agatatggga	aagttttcag	aggaaataag	900
49	tactaaaaat	cccagctggc	agggggccaa	ggagtcattc	tctactccga	ccctgctgac	960
51	tactttgtct	ctgggggtgaa	gtcctatcca	gatggttgga	atcttctctg	aggtggtgtc	1020
53	cagcgtggaa	atatectaaa	tctgaatggt	gcaggagacc	ctctcacacc	aggttaccca	1080
55	gcaaatgaat	atgcttatag	gcgtggaatt	gcagaggctg	ttggtcttcc	aagtattcct	1140
57	gttcatccaa	ttggatacta	tgatgcacag	aagctcctag	aaaaaatggg	tggctcagca	1200
59	ccaccagata	gcagctggag	aggaagtctc	aaagtgcctc	acaatgttgg	acctggcttt	1260
61	actggaact	tttctacaca	aaaagtcaag	atgcacatcc	actctaccaa	tgaagtgaca	1320
63	agaatttaca	atgtgatagg	tactctcaga	ggagcagtg	aaccagacag	atatgtcatt	1380
65	ctgggaggtc	accgggactc	atgggtgttt	ggtggtattg	accctcagag	tggagcagct	1440
67	gttgttcacg	aaattgtgag	gagctttgga	acactgaaaa	aggaagggtg	gagacctaga	1500
69	agaacaattt	tgtttgcaag	ctgggatgca	gaagcaattg	gtcttcttgg	ttctactgag	1560
71	tgggcagagg	agaattcaag	actccttcaa	gagcgtggcg	tggcttatat	taatgctgac	1620
73	tcctctatag	aaggaaacta	cactctgaga	gttgattgta	caccgctgat	gtacagcttg	1680
75	gtacacaacc	taacaaaaga	gctgaaaagc	cctgatgaag	gctttgaagg	caaatctctt	1740
77	tatgaaagtt	ggactaaaaa	aagtccttcc	ccagagttca	gtggcatgcc	caggataagc	1800
79	aaattgggat	ctggaaatga	ttttgaggtg	ttcttccaac	gacttggaat	tgcttcaggc	1860
81	agagcacggt	atactaaaaa	ttgggaaaca	aacaaattca	gcggctatcc	actgtatcac	1920
83	agtgtctatg	aaacatatga	gttggtggaa	aagttttatg	atccaatgtt	taaatatcac	1980
85	ctcactgtgg	cccaggttcg	aggagggatg	gtgtttgagc	tagccaattc	catagtgtct	2040
87	ccttttgatt	gtcgagatta	tgtgttagtt	ttaagaaaag	atgctgacaa	aatctacagt	2100

Does Not Comply
Corrected Diskette Needed
see Add 1 & Add 2

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Input Set : A:\41426-A-PCT-US.txt

Output Set: N:\CRF3\07202001\H403803A.raw

```

89 atttctatga aacatccaca ggaaatgaag acatacagtg tatcatttga ttcacttttt 2160
91 tctgcagtaa agaattttac agaaattgct tccaagttca gtgagagact ccaggacttt 2220
93 gacaaaagca acccaatagt attaagaatg atgaatgac aactcatgtt tctggaaaga 2280
95 gcattttattg atccattagg gttaccagac aggccttttt ataggcatgt catctatgct 2340
97 ccaagcagcc acaacaagta tgcaggggag tcattcccag gaatttatga tgctctgttt 2400
99 gatattgaaa gcaaagtggg cccttccaag gcctggggag aagtgaagag acagatttat 2460
101 gttgcagcct tcacagtgcg ggcagctgca gagactttga gtgaagtagc ctaagaggat 2520
103 tcttttagaga atccgtattg aatttgtgtg gtatgtcact cagaaagaat cgtaatgggt 2580
105 atattgataa attttaaaat tggatatatt gaaataaagt tgaatattat atataaaaaa 2640
107 aaaaaaaaaa aaa 2653
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 750
112 <212> TYPE: PRT
113 <213> ORGANISM: human
115 <400> SEQUENCE: 2
117 Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
118 1 5 10 15
120 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
121 20 25 30
123 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
124 35 40 45
126 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
127 50 55 60
129 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
130 65 70 75 80
132 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
133 85 90 95
135 Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
136 100 105 110
138 Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
139 115 120 125
141 Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
142 130 135 140
144 Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
145 145 150 155 160
147 Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
148 165 170 175
150 Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
151 180 185 190
153 Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
154 195 200 205
156 Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
157 210 215 220
159 Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
160 225 230 235 240
162 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
163 245 250 255
165 Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
166 260 265 270

```

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```

168 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
169      275      280      285
171 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
172      290      295      300
174 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
175 305      310      315      320
177 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
178      325      330      335
180 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
181      340      345      350
183 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
184      355      360      365
186 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
187      370      375      380
189 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
190 385      390      395      400
192 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
193      405      410      415
195 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
196      420      425      430
198 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
199      435      440      445
201 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
202      450      455      460
204 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
205 465      470      475      480
207 Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
208      485      490      495
210 Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
211      500      505      510
213 Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
214      515      520      525
216 Lys Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
217      530      535      540
219 Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
220 545      550      555      560
222 Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
223      565      570      575
225 Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
226      580      585      590
228 Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
229      595      600      605
231 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
232      610      615      620
234 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
235 625      630      635      640
237 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
238      645      650      655
240 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu

```

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```

241          660          665          670
243 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
244          675          680          685
246 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
247          690          695          700
249 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
250 705          710          715          720
252 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
253          725          730          735
255 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
256          740          745          750
258 <210> SEQ ID NO: 3
259 <211> LENGTH: 8
260 <212> TYPE: PRT
261 <213> ORGANISM: human
263 <400> SEQUENCE: 3
265 Ser Leu Tyr Glu Ser Trp Thr Lys
266 1          5
268 <210> SEQ ID NO: 4
269 <211> LENGTH: 15
270 <212> TYPE: PRT
271 <213> ORGANISM: human
273 <220> FEATURE:
W--> 274 <221> NAME/KEY: misc.
275 <222> LOCATION: (1)..(15)
276 <223> OTHER INFORMATION: x=unknown
279 <400> SEQUENCE: 4
W--> 281 Ser Tyr Pro Asp Gly Xaa Xaa Leu Pro Gly Gly Gly Val Gln Arg
282 1          5          10          15
284 <210> SEQ ID NO: 5
285 <211> LENGTH: 7
286 <212> TYPE: PRT
287 <213> ORGANISM: human
289 <400> SEQUENCE: 5
291 Phe Tyr Asp Pro Met Phe Lys
292 1          5
294 <210> SEQ ID NO: 6
295 <211> LENGTH: 9
296 <212> TYPE: PRT
297 <213> ORGANISM: human
299 <400> SEQUENCE: 6
301 Ile Tyr Asn Val Ile Gly Thr Leu Lys
302 1          5
304 <210> SEQ ID NO: 7
305 <211> LENGTH: 22
306 <212> TYPE: PRT
307 <213> ORGANISM: human
309 <220> FEATURE:
W--> 310 <221> NAME/KEY: misc

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Input Set : A:\41426-A-PCT-US.txt

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```

311 <222> LOCATION: (1)..(22)
312 <223> OTHER INFORMATION: x=unknown
315 <400> SEQUENCE: 7
W--> 317 Phe Leu Tyr Xaa Xaa Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln
318 1 5 10 15
320 Asn Phe Gln Leu Ala Lys
321 20
323 <210> SEQ ID NO: 8
324 <211> LENGTH: 17
325 <212> TYPE: PRT
326 <213> ORGANISM: human
328 <400> SEQUENCE: 8
330 Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Asp Val
331 1 5 10 15
333 Lys
336 <210> SEQ ID NO: 9
337 <211> LENGTH: 17
338 <212> TYPE: PRT
339 <213> ORGANISM: human
341 <400> SEQUENCE: 9
343 Pro Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val
344 1 5 10 15
346 Lys
349 <210> SEQ ID NO: 10
350 <211> LENGTH: 15
351 <212> TYPE: PRT
352 <213> ORGANISM: human
354 <400> SEQUENCE: 10
356 Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
357 1 5 10 15
359 <210> SEQ ID NO: 11
360 <211> LENGTH: 19
361 <212> TYPE: PRT
362 <213> ORGANISM: human
364 <400> SEQUENCE: 11
366 Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile
367 1 5 10 15
369 Glu Ser Lys
372 <210> SEQ ID NO: 12
373 <211> LENGTH: 22
374 <212> TYPE: PRT
375 <213> ORGANISM: human
377 <220> FEATURE:
W--> 378 <221> NAME/KEY: misc.
379 <222> LOCATION: (1)..(22)
380 <223> OTHER INFORMATION: x=unknown
383 <400> SEQUENCE: 12
W--> 385 Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Xaa Xaa Gly
386 1 5 10 15

```

FYI.

Use of 'n' and/or 'Xaa' has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using 'n' or 'Xaa'.

Add 1

<210> 13

<211> 17

<212> DNA

<213> artificial;primer

<220>

<221> misc.

<222> (1)..(16)

<223> n=unknown

<400> 13

ttytaygayc cnatgtt

<210> 14

<211> 17

<212> DNA

<213> artificial;primer

<220>

<221> misc

<222> (1)..(16)

<223> n=unknown

<400> 14

aacatnggrt crtaraa

<210> 15

<211> 17

<212> DNA

<213> artificial;primer

<220>

<221> misc.

see item # 10 on
ERROR summary
sheet
↓

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

17

17

ADD 2

<210> 30

<211> 27

<212> DNA

<213> artificial

— see item # 11 on ERROR
Summary SHEET.

<400> 30

acggagcaaa actttcagct tgcaaag

27

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/403,803A

DATE: 07/20/2001

TIME: 13:26:04

Input Set : A:\41426-A-PCT-US.txt

Output Set: N:\CRF3\07202001\H403803A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:274 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:310 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:378 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:394 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:397 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:409 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:412 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:424 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:427 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:439 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:442 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:454 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:457 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:469 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:472 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:478 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:484 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:487 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:499 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:502 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:514 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:516 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:516 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:523 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:525 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:525 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:532 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:535 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:547 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:550 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:562 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:565 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:577 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26

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Input Set : A:\41426-A-PCT-US.txt

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L:580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:595 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:634 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:669 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
L:681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:697 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:699 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:699 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:706 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:708 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:708 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:716 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:718 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:718 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:725 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:727 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:727 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:734 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:736 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:736 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

RECEIVED

SEP 11 2001

TECH CENTER 1600/2900

Raw Sequence Listing Error Summary

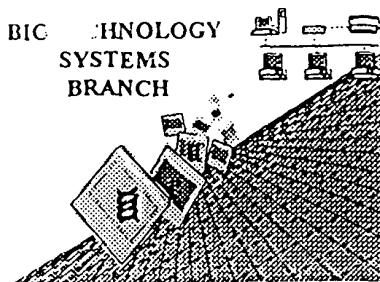
ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 08/403,803A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220> Sequence(s) 30 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

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<http://www.uspto.gov/web/offices/pac/checker>